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(54) **D-Sorbitol dehydrogenase gene**

(57) A DNA comprising a nucleotide sequence which encodes a protein as defined by (a) or (b) and having sorbitol dehydrogenase activity:

(a) a protein having the amino acid sequence from the position 1 to 716 of the sequence described in SEQ ID NO: 2, or

(b) a protein derived from the protein of (a) by substitution, deletion, insertion or addition of one or more amino acids in the amino acid sequence defined in (a), vectors, comprising such DNAs, hosts transformed by such vectors, a process for the preparation of such proteins and their use.

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Description

[0001] The present invention relates to a novel DNA coding for sorbitol dehydrogenase of a microorganism belonging to acetic acid bacteria including the genus *Gluconobacter* and the genus *Acetobacter*, an expression vector containing the said DNA, and recombinant organisms containing the said expression vector. Furthermore, the present invention relates to a process for producing recombinant D-sorbitol dehydrogenase and a process for producing L-sorbose by utilizing the said recombinant enzymes or recombinant organisms containing the said expression vector.

[0002] L-Sorbose is an important intermediate in the actual industrial process of vitamin C production, which is mainly practiced by Reichstein method (Helvetica chimica Acta, 17: 311, 1934). In the process, the only microbial conversion is the L-sorbose production from D-sorbitol by *Gluconobacter* or *Acetobacter* strains. The conversion is considered to be carried out by NAD/NADP independent D-sorbitol dehydrogenase (SLDH). L-Sorbose is also a well known substrate in the art for microbiologically producing 2-keto-L-gulonic acid, which is a useful intermediate in the production of vitamin C.

[0003] It is known that there are NAD/NADP-independent D-sorbitol dehydrogenase which catalyzes the oxidation of D-sorbitol to L-sorbose. The said D-sorbitol dehydrogenase was isolated and characterized from *Gluconobacter suboxydans* var α IFO 3254 (E. Shinagawa et al., Agric Biol. Chem., 46: 135-141, 1982), and found to consist of three subunits with the molecular weight of 63 kDa, 51 kDa, and 17 kDa; the largest subunit is dehydrogenase containing FAD as a cofactor, the second one is cytochrome c AB/vs / 26.6.98 and the smallest one is a protein with unknown function; and shows its optimal pH at 4.5. Such SLDH was also purified and characterized from *G. suboxydans* ATCC 621 (KCTC 2111) (E-S Choi et al., FEMS Microbiol. Lett. 125:45-50, 1995) and found to consist of three subunits with the molecular weight of 75 kDa, 50 kDa, and 14 kDa; the large subunit is dehydrogenase containing pyrroloquinoline quinone (PQQ) as a cofactor, the second one is cytochrome c and the small one is a protein with unknown function. The inventors also purified and characterized the NAD/NADP-independent SLDH from *G. suboxydans* IFO 3255 (T. Hoshino et al., EP 728840); the SLDH consists of one Kind of subunit with the molecular weight of 79.0 +/- 0.5 kDa and shows its optimal pH at 6 to 7 and shows dehydrogenase activity on mannitol and glycerol as well as on D-sorbitol.

[0004] Although several SLDHs have been purified, their genes have not been cloned yet. It is useful to clone the SLDH gene for efficient production of the SLDH enzyme and for constructing recombinant organism having enhanced SLDH activity to improve the production yield of L-sorbose. It is also useful to introduce the said SLDH gene into desired organisms, for example, *Gluconobacter* converting L-sorbose to 2-keto-L-gulonic acid for constructing recombinant microorganisms which directly produce 2-keto-L-gulonic acid from D-sorbitol.

[0005] The present invention provides a nucleotide sequence (gene) coding for D-sorbitol dehydrogenase (SLDH) originating from a microorganism belonging to acetic acid bacteria including the genus *Gluconobacter* and the genus *Acetobacter*; a DNA molecule comprising said nucleotide sequence as well as a combination of the said DNA with a DNA comprising a nucleotide sequence of a protein functional in activating the said SLDH in vivo, expression vectors carrying the DNA comprising SLDH nucleotide sequence or the said combination of the DNAs; recombinant organisms carrying the expression vectors; a process for producing the recombinant SLDH; and a process for producing L-sorbose by utilizing the recombinant SLDH or the recombinant organisms.

[0006] The present invention is also directed to functional derivatives of the present case. Such functional derivatives are defined on the basis of the amino acid sequences of the present invention by addition, insertion, deletion and/or substitution of one or more amino acid residues of such sequences wherein such derivatives still have SLDH activity measured by an assay known in the art or specifically described herein. Such functional derivatives can be made either by chemical peptide synthesis known in the art or by recombinant means on the basis of the DNA sequences as disclosed herein by methods known in the state of the art and disclosed e.g. by Sambrook et al. (Molecular Cloning, Cold Spring Harbour Laboratory Press, New York, USA, second edition 1989). Amino acid exchanges in proteins and peptides which do not generally alter the activity of such molecules are known in the state of the art and are described, for example, by H. Neurath and R. L. Hill in "The Proteins" (Academic Press, New York, 1979, see especially Figure 6, page 14). The most commonly occurring exchanges are: Ala/Ser, Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, Asp/Gly as well as these in reverse.

[0007] Furthermore the present invention is directed to DNA sequences encoding the polypeptides with SLDH activity and polypeptides functional in activating the said SLDH in vivo as disclosed e.g. in the sequence list as SEQ ID NO:2 and NO:3 as well as their complementary strands, or those which include these sequences, DNA sequences which hybridize under standard conditions with such sequences or fragments thereof and DNA sequences, which because of the degeneration of the genetic code, do not hybridize under standard conditions with such sequences but which code for polypeptides having exactly the same amino acid sequence.

[0008] "Standard conditions" for hybridization mean in this context the conditions which are generally used by a man skilled in the art to detect specific hybridization signals and which are described, e. g. by Molecular Cloning, Cold Spring Harbour Laboratory Press, New York, USA, second edition 1989, or preferably so called stringent hybridization and stringent washing conditions a man skilled in the art is familiar with and which are described, e. g. in Sambrook et al.

(s. a.).

In the following a brief description of the drawings is given.

Figure 1 illustrates the partial amino acid sequences of SLDH polypeptide and oligonucleotides. The amino acid sequences in boldface in the figure were used for synthesizing two oligonucleotide sequences (S7 and S6R) for PCR. Arrow shows direction of DNA synthesis. All primers were degenerate DNA mixtures having bias for *Gluconobacter* codon usage.

Figure 2 illustrates a restriction map of the SLDH gene cloned in the present invention and the genetic structure of the DNA region encoding SLDH and ORF2.

Figure 3 illustrates the nucleotide sequence encoding SLDH and ORF2 with upstream and downstream sequences and illustrates deduced amino acid sequences of SLDH and ORF2. Figure 3 also illustrates putative ribosome-binding sites (SD sequences) of SLDH and ORF2 genes and the possible transcription terminator sequences.

Figure 4 illustrates the steps for constructing plasmids pTNB114, pTNB115, and pTNB116 for the expression of SLDH and/or ORF2 genes in *E. coli* under the control of lac promoter.

Figure 5 illustrates the steps for constructing plasmids pTNB110 which carries ORF2 and SLDH genes under the control of common pA promoter (described below in Example 6) and pTNB143 which carries ORF2 gene under the control of pA located adjacent to the gene in the upstream and SLDH gene under the control of another pA promoter located adjacent to the SLDH gene in its upstream.

[0009] The inventors have isolated SLDH gene together with a gene functionable in developing SLDH activity in vivo by DNA recombinant techniques and determined the nucleotide sequences.

[0010] The present invention provides DNA sequences encoding *Gluconobacter* SLDH and a gene functionable in developing SLDH activity in vivo herein after referred to as ORF2 gene, expression vectors containing the said DNA for SLDH and host cells carrying the said expression vectors.

[0011] Briefly, the SLDH and/or ORF2 gene(s), the DNA molecule containing the said gene(s), the recombinant expression vector and the recombinant organism utilized in the present invention can be obtained by the following steps:

(1) Isolating chromosomal DNA from the microorganisms which can provide SLDH activity that converts D-sorbitol to L-sorbose and constructing the gene library with the chromosomal DNA in an appropriate host cell, e. g. *E. coli*.

(2) Cloning SLDH and/or ORF2 gene(s) from a chromosomal DNA by colony-, plaque-, or Southern-hybridization, PCR (polymerase chain reaction) cloning, Western-blot analysis and the like.

(3) Determining the nucleotide sequence of the SLDH and/or ORF2 gene(s) obtained as above by conventional methods to select DNA molecule containing said SLDH and/or ORF2 gene(s) and constructing the recombinant expression vector on which SLDH and/or ORF2 gene(s) can express efficiently.

(4) Constructing recombinant organisms carrying SLDH and/or ORF2 gene(s) by an appropriate method for introducing DNA into host cell, e. g. transformation, transduction, transconjugation and/or electroporation.

[0012] The materials and the techniques used in the above aspect of the present invention are exemplified in details as follows:

[0013] A total chromosomal DNA can be purified by a procedure well known in the art. The aimed gene can be cloned in either plasmid or phage vectors from a total chromosomal DNA typically by either of the following illustrative methods:

(i) The partial amino acid sequences are determined from the purified proteins or peptide fragments thereof. Such whole protein or peptide fragments can be prepared by the isolation of such a whole protein or by peptidase-treatment from the gel after SDS-polyacrylamide gel electrophoresis. Thus obtained protein or fragments thereof are applied to protein sequencer such as Applied Biosystems automatic gas-phase sequencer 470A. The amino acid sequences can be utilized to design and prepare oligonucleotide probes and/or primers with DNA synthesizer such as Applied Biosystems automatic DNA sequencer 381A. The said probes can be used for isolating clones carrying the objective gene from a gene library of the strain carrying the objective gene with the aid of Southern-, colony- or plaque-hybridization.

(ii) Alternatively, for the purpose of selecting clones expressing aimed protein from the gene library, immunological methods with antibody prepared against the aimed protein can be applied.

(iii) The DNA fragment of the aimed gene can be amplified from the total chromosomal DNA by PCR method with a set of primers, i.e. two oligonucleotides synthesized according to the amino acid sequences determined as above. Then a clone carrying the aimed-whole gene can be isolated from the gene library constructed, e.g. in *E. coli* by Southern-, colony-, or plaque-hybridization with the PCR product obtained above as the probe.

(iv) A further alternative way of the cloning is screening of the clone complementing SLDH-deficient strain constructed by conventional mutation with chemical mutagenesis or by recombinant DNA techniques e.g. with transposon Tn5 to disrupt aimed gene.

[0014] DNA sequences which can be made by the polymerase chain reaction by using primers designed on the basis of the DNA sequences disclosed therein by methods known in the art are also an object of the present invention. It is understood that the DNA sequences of the present invention can also be made synthetically as described, e.g. in EP 747 483.

[0015] Above mentioned antibody can be prepared with purified SLDH protein or its peptide fragment as an antigen by such method described in Methods in Enzymology, vol. 73, p 46, 1981.

[0016] Once a clone carrying the desired gene is obtained, the nucleotide sequence of the aimed gene can be determined by a well known method such as dideoxy chain termination method with M13 phage (Sanger F. et al., Proc. Natl. Acad. Sci. USA, 74:5463-5467, 1977).

[0017] The desired gene expressing the D-sorbitol dehydrogenase activity of the present invention is illustrated in Fig. 2 and Fig. 3. This specific gene encodes the SLDH enzyme having 716 amino acid residues together with a signal peptide of 24 amino acid residues. The inventors found an open reading frame just upstream of the above SLDH structure gene and designated it as ORF2. This ORF2 gene encodes a protein having 126 amino acid residues, and was suggested to be functional in providing the desired enzymatic activity to the recombinant SLDH of the present invention, in particular when the said SLDH is expressed in a host cell of a different genus from acetic acid bacteria.

[0018] To express the desired gene/nucleotide sequence isolated from acetic acid bacteria including genus *Gluconobacter* and genus *Acetobacter* efficiently, various promoters can be used; for example, the original promoter of the gene, promoters of antibiotic resistance genes such as kanamycin resistant gene of Tn5 (D. E. Berg, and C. M. Berg, 1983, Bio/Technology 1:417-435), ampicillin resistant gene of pBR322, and β -galactosidase of *E. coli* (*lac*), *trp*-, *tac*-, *trc*-promoter, promoters of lambda phage and any promoters which can be functional in a host organism. For this purpose, the host organism can be selected from microorganisms including bacteria such as *Escherichia coli*, *Pseudomonas putida*, *Acetobacter xylinum*, *Acetobacter pasteurianus*, *Acetobacter aceti*, *Acetobacter hansenii*, and *Gluconobacter albidus*, *Gluconobacter capsulatus*, *Gluconobacter cerinus*, *Gluconobacter dioxyaceticus*, *Gluconobacter gluconicus*, *Gluconobacter industrius*, *Gluconobacter melanogenus*, *Gluconobacter nonoxygluconicus*, *Gluconobacter oxydans*, e.g. *Gluconobacter oxydans* DSM 4025, which had been deposited as DSM 4025 on March 17, 1987 under the conditions of the Budapest Treaty at the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, BRD, *Gluconobacter oxydans* subsp. *sphaericus*, *Gluconobacter roseus*, *Gluconobacter rubiginosus*, *Gluconobacter suboxydans*, mammalian cells and plant cells.

[0019] For expression, other regulatory elements, such as a Shine-Dalgarno (SD) sequence (for example, AGGAGG etc. including natural and synthetic sequences operable in the host cell) and a transcriptional terminator (inverted repeat structure including any natural and synthetic sequence operable in the host cell) which are operable in the host cell into which the coding sequence will be introduced can be used with the above described promoters.

[0020] For the expression of membrane-bound polypeptides, like the SLDH protein of the present invention, a signal peptide, which contains usually 15 to 50 amino acid residues and is totally hydrophobic, is preferably associated. A DNA encoding a signal peptide can be selected from any natural and synthetic sequence operable in the desired host cell.

[0021] A wide variety of host/cloning vector combinations may be employed in cloning the double-stranded DNA. The cloning vector is generally a plasmid or phage which contains a replication origin, regulatory elements, a cloning site including a multi-cloning site and selection markers such as antibiotic resistance genes including resistance genes for ampicillin, tetracycline, kanamycin, streptomycin, gentamicin, spectinomycin etc.

[0022] Preferred vectors for the expression of the gene of the present invention in *E. coli* is selected from any vectors usually used in *E. coli*, such as pBR322 or its derivatives including pUC18 and pBluescript II (Stratagene Cloning Systems, CA, USA), pACYC177 and pACYC184 (J. Bacteriol., 134:1141-1156, 1978) and their derivatives, and a vector derived from a broad host range plasmid such as RK2 (C. M. Thomas, Plasmid 5: 10, 1981) and RSF1010 (P. Guerry et al., J. Bacteriol. 117: 619-630, 1974). A preferred vector for the expression of the nucleotide sequence of the present invention in bacteria including *Gluconobacter*, *Acetobacter* and *P. putida* is selected from any vectors which can replicate in *Gluconobacter*, *Acetobacter* and/or *P. putida*, as well as in a preferred cloning organism such as *E. coli*. The

preferred vector is a broad-host-range vector such as a cosmid vector like pVK100 (V. C. Knauf et al., Plasmid 8: 45-54, 1982) and its derivatives and RSF1010. Copy number and stability of the vector should be carefully considered for stable and efficient expression of the cloned gene and also for efficient cultivation of the host cell carrying the cloned gene. DNA molecules containing transposable elements such as Tn5 can be also used as a vector to introduce the desired gene into the preferred host, especially on a chromosome. DNA molecules containing any DNAs isolated from the preferred host together with the gene of the present invention is also useful to introduce this gene into the preferred host, especially on a chromosome. Such DNA molecules can be transferred to the preferred host by applying any of a conventional method, e.g. transformation, transduction, transconjugation or electroporation, which are well known to those skilled in the art, considering the nature of the host and the DNA molecule.

[0023] Useful hosts may include microorganisms, mammalian cells, and plant cells and the like. As a preferable microorganism, there may be mentioned bacteria such as *E. coli*, *P. putida*, *A. xylinum*, *A. pasteurianus*, *A. aceti*, *A. hansenii*, *Gluconobacter albidus*, *Gluconobacter capsulatus*, *Gluconobacter cerinus*, *Gluconobacter dioxyceticus*, *Gluconobacter gluconicus*, *Gluconobacter industrius*, *Gluconobacter melanogenus*, *Gluconobacter nonoxygluconicus*, *Gluconobacter oxydans*, *Gluconobacter oxydans subsp. sphaericus*, *Gluconobacter roseus*, *Gluconobacter rubiginosus*, *Gluconobacter suboxydans*, and any bacteria which are capable of expressing recombinant SLDH and/or ORF2 gene(s). Functional equivalents, subcultures, mutants and variants of said microorganism can be also used in the present invention. A preferred strain is *E. coli* K12 or its derivatives, *P. putida*, *Gluconobacter*, or *Acetobacter* strains.

[0024] The SLDH and/or ORF2 gene(s)/nucleotide sequences provided in this invention are ligated into a suitable vector containing a regulatory region such as a promoter, a ribosomal binding site and a transcriptional terminator operable in the host cell described above with a well-known methods in the art to produce an expression vector. When the SLDH and ORF2 genes are cloned in combination, the two genes can be cloned either in tandem or separately on the same plasmid and also on the chromosomal DNA. Figures 4 and 5 exemplifies the form of the combined cloning of SLDH and ORF2 genes on the plasmid. One may clone also one gene on a plasmid and the other one on chromosomal DNA.

[0025] To construct a recombinant microorganism carrying a recombinant expression vector, various gene transfer methods including transformation, transduction, conjugal mating (Chapters 14 and 15, Methods for general and molecular bacteriology, Philipp Gerhardt et al. ed., American Society for Microbiology, 1994), and electroporation can be used. The method for constructing a recombinant organism may be selected from the methods well-known in the field of molecular biology. Usual transformation systems can be used for *E. coli*, *Pseudomonas*, *Gluconobacter* and *Acetobacter*. A transduction system can also be used for *E. coli*. Conjugal mating system can be widely used in Gram-positive and Gram-negative bacteria including *E. coli*, *P. putida* and *Gluconobacter*. A preferred conjugal mating is disclosed in WO89/06688. The conjugation can occur in liquid medium or on a solid surface. The preferred recipient for SLDH and/or ORF2 production is selected from *E. coli*, *P. putida*, *Gluconobacter* and *Acetobacter*. To the recipient for conjugal mating, a selective marker is usually added; for example, resistance against nalidixic acid or rifampicin is usually selected. Natural resistance can be also used; e.g. resistance against polymyxin B is useful for many *Gluconobacters*.

[0026] The present invention provides recombinant SLDH. One can increase the production yield of the SLDH enzyme by introducing the gene of SLDH provided by the present invention into organisms including acetic acid bacteria including the genus *Gluconobacter* and the genus *Acetobacter*. One can also produce active SLDH in microorganisms beside *Gluconobacter* by using the SLDH gene of the present invention in combination with the ORF2 gene of the present invention. The recombinant SLDH can be immobilized on a solid carrier for solid phase enzyme reaction? The present invention also provides recombinant organisms. One can produce L-sorbose from D-sorbitol with the recombinant organisms. One can also produce L-sorbose from D-sorbitol even in a host organism beside acetic acid bacteria by introducing the SLDH gene in combination with the ORF2 gene of the present invention.

Examples

Example 1. Determination of amino acid sequences of SLDH

(1) N-terminal amino acid sequence analyses of lysylendopeptidase-treated SLDH polypeptides

[0027] Partial amino acid sequences of peptides No. 1, 3 and 8 prepared from SLDH protein were determined (Fig. 1; SEQ ID NO:4 to 6). Purified SLDH of *G. suboxydans* IFO 3255 (T. Hoshino et al., EP 728840) was digested with lysylendopeptidase; the reaction mixture (25 ml) contained 1.2 mM of lysylendopeptidase and 3 nmol of the SLDH protein in 100 mM Tris-HCl buffer, pH9.0, and the reaction was carried out at 37°C for 15 hours. The resulting peptide fragments were separated by HPLC (column: protein C-4, VYDAC, California, USA) with acetonitrile/isopropanol gradient in 0.1% TFA at a flow rate of 1.0 ml/min. Elution of the peptides was monitored by UV absorbance at 214 nm, and the

peak fractions were collected manually and subjected to N-terminal amino acid sequence analysis with an amino acid sequencer (Applied Biosystems model 470A, The Perkin Elmer Corp., Conn., USA).

Example 2. Cloning of partial SLDH gene by PCR

[0028] PCR was conducted with chromosomal DNA of *G. suboxydans* IFO 3255 and degenerate oligonucleotide DNA primers, s7 and s6R whose sequences are shown in Fig. 1. The PCR amplification was carried out with thermostable polymerase Amplitaq (Perkin-Elmer, Roche Molecular Systems Inc., NJ, USA), using a thermal cycler (ZYMOREACTOR II AB-1820, ATTO, Tokyo, Japan). The following reaction mixture (50 µl) was used for PCR: 200 µM of dNTPs, 10 ~ 20 pmol of each primer (54 ~ 288 degeneracy), 6 ng of chromosomal DNA of *G. suboxydans* IFO 3255 and 0.5 unit of the DNA polymerase in the buffer provided from the supplier. The reaction consisted of 30 cycles of 1) denaturation step at 94°C for 1 min; 2) annealing step at 48°C for 1 min; 3) synthesis step at 72°C for 2 min. Consequently, 1.6 kb DNA was amplified and cloned in *E. coli* vector, pUC57/T (MBI Fermentas, Vilnius, Lithuania), which has 3'Ö-ddT-tailed ends for direct ligation of an amplified DNA fragment to obtain a recombinant plasmid pMT20. The cloned DNA was subjected to nucleotide sequencing by the method of dideoxy-chain termination (F. Sanger et al, Proc. Natl. Acad. Sci. USA, 74:5463-5467, 1977); the 1.6 kb fragment encoded the peptides No. 3 and No. 8.

Example 3. Complete cloning of the SLDH gene

(1) Construction of gene library of *G. suboxydans* IFO 3255

[0029] The chromosomal DNA of *G. suboxydans* IFO 3255 was prepared from the cells grown on MB agar plate for 2 days. The chromosomal DNA (160 µg) was partially digested with 20 units of *Eco* RI in 500 µl of reaction mixture. Portions of the sample were withdrawn at 5, 10, 15, 30, and 60 minutes and the degree of the digestion was detected by agarose gel electrophoresis. Former four portions which contained partially-digested DNA fragments were combined and subjected to preparative gel electrophoresis (agarose: 0.6%). Fragments of 15 - 35 kb were cut out and electroeluted from the gel. The eluate was filtered and precipitated with sodium acetate and ethanol at -80°C. The DNA fragments were collected by centrifugation and suspended in 200 µl of 10 mM Tris-HCl, pH8.0, buffer containing 1 mM EDTA.

[0030] In parallel, 1.8 µg of a cosmid vector pVK100 was completely digested with *Eco* RI and treated with calf intestine alkaline phosphatase. The linearized and dephosphorylated pVK100 was ligated with 15 - 35 kb *Eco* RI fragments of the chromosomal DNA of *G. suboxydans* IFO 3255 (5 µg) with the ligation kit (Takara Shuzo, Kyoto, Japan) in 20 separate tubes under the condition recommended by the supplier to obtain highly polymerized DNA. The ligated DNA was then used for in vitro packaging according to the method described by the supplier (Amersham Japan). The resulting phage particles were used to infect *E. coli* ED8767, a host for the genomic library. Consequently, 4,271 colonies were obtained and all of the colonies tested (20 colonies) possessed the insert DNAs with the average size of about 25 kb.

(2) Colony hybridization to obtain complete SLDH gene

[0031] The cosmid library described above was screened to isolate the clone carrying complete SLDH gene by colony hybridization method with ³²P-labeled 1.6 kb DNA of pMT20. One clone was isolated and designated pSLII, which carry about 25 kb insert in pVK100 vector. From the pSLII, 6.2 kb *Pst* I fragment was isolated and cloned into pUC18 to obtain plasmid pUSLIIP. The 6.2 kb *Pst* I fragment containing ORF2 and SLDH genes was isolated from pUSLIIP and subcloned into pCRII vector (Invitrogen Corporation, CA, USA) to produce pCRSLIIP. From the resulting plasmid, the DNA fragment containing the 6.2 kb *Pst* I fragment was isolated as *Hind* III-*Xho* I fragment and cloned between *Hind* III and *Xho* I sites of pVK100 to obtain pVKSLIIP.

(3) Expression of SLDH gene in *E. coli*

[0032] To confirm whether 6.2 kb *Pst* I-fragment encodes the aimed SLDH, cells of *E. coli* JM109 carrying pUSLIIP was subjected to Western-blot analysis with anti-SLDH antibody as described above. Immuno-positive proteins with a molecular weight of about 80 kDa were observed in the transformant, indicating that the *Pst* I-fragment encodes the polypeptides with the molecular weight of the intact SLDH (79 kDa +/- 0.5 kDa).

(4) Construction of SLDH-deficient *Gluconobacter*, strain 26A11, as the test strain for SLDH-activity complementation

[0033] Transposon Tn5 mutagenesis was performed with *G. melanogenus* IFO 3293 as the parent. Tn5, a transposable element coding for *Kmr*, causes null mutations at random on DNA of its host organism and widely used as a muta-

gen in Gram-negative bacteria. The IFO 3293 was selected as the parent in the following reasons: (i) it produced L-sorbose from D-sorbitol, (ii) it showed immuno-positive polypeptide of about 80 kDa in Western-blot analysis with the antibody prepared against SLDH purified from *G. suboxydans* IFO 3255 and (iii) its frequency for generating Tn5 mutants was much higher than that of *G. suboxydans* IFO 3255.

[0034] *G. melanogenus* IFO 3293 was cultivated in a test tube containing 5 ml of the MB medium containing 25 g/l of mannitol, 5 g/l of yeast extract (Difco Laboratories,), 3 g/l of Bactopepton (Difco) at 30°C overnight. *E. coli* HB101 (pRK2013) [D. H. Figurski, Proc. Natl. Acad. Sci. USA 76: 1648 - 1652, 1979] and *E. coli* HB101 (pSUP2021) [R. Simon, et al., BIO/TECHNOL. 1:784-791, 1983] were cultivated in test tubes containing 5 ml of LB medium with 50 µg/ml of kanamycin at 37°C overnight. The cells were separately collected by centrifugation and suspended in the half volume of MB medium. The each cell suspension was mixed in the ratio of 1:1:1 and the mixture was placed on the nitrocellulose filter on the surface of MB agar plate. The plate was incubated at 27°C overnight and the resulting cells on the filter was scraped, suspended in the appropriate volume of MB medium and spread on the selection plate (MPK plate), MB containing 10 µg/ml of polymyxin B and 50 µg/ml of kanamycin. The MPK plate was incubated at 27°C for 3 to 4 days.

[0035] The resulting 3,436 Tn5 mutants were subjected to the immuno-dot blot screening with the anti-SLDH antibody. The cells of each strain were independently suspended in 50 µl Laemmli buffer consisting of 62.5 mM Tris-HCl (pH6.5), 10% glycerol, 2% SDS and 5% β-mercaptoethanol in 96-well microtiter plate and incubated at 60°C for 2 hours. The Cell Free Extracts (CFEs) were stamped on the nitrocellulose filter and the immuno-positive samples in the CFEs were screened with AP conjugate substrate Kit (Bio-RAD Laboratories, Richmond, Calif., USA). As a result, only one strain 26A11 without positive signal in the immuno-dot blot screening was obtained.

[0036] SLDH-deficiency of the strain 26A11 was confirmed by Western-blot analysis; it expressed at most 1/500 amount of SLDH compared with its parent strain. 26A11 was not a complete SLDH-deficient strain but the strain with SLDH gene repressed by Tn5 insertion; the insertion site was found to be close to the C-terminus by determining the nucleotide sequence around Tn5-insertion point. Next, a resting cell reaction was conducted to examine the whole SLDH activity in 26A11 and the wild *Gluconobacter* strains. In the potassium phosphate buffer 100 mM (pH7.0) containing 2% D-sorbitol, 26A11 slightly converted D-sorbitol to L-sorbose, whereas the wild strains IFO 3293 and IFO 3255 completely did it in 39.5 hr at 30°C.

(5) Expression of SLDH gene in 26A11

[0037] To confirm the SLDH activity of the SLDH clones obtained, complementation test was conducted. Plasmids pSLII and pVKSLIIP were introduced into 26A11 by a conjugal mating. The transconjugant carrying pSLII or pVKSLIIP restored the activity of SLDH in a mini-resting cell reaction and showed immuno-reactive polypeptide of about 80 kDa in Western-blot analysis.

(6) Nucleotide sequencing of the SLDH gene

[0038] Plasmid pUSLIIP was used for nucleotide sequencing of SLDH and ORF2 genes. Determined nucleotide sequence (SEQ ID NO: 1; 3,481 bp) revealed that ORF of SLDH gene (2,223 bp, nucleotide No. 572 to 2794 in SEQ ID NO: 1) encoded the polypeptide of 740 amino acid residues (SEQ ID NO: 2), in which there were three amino acid sequences (Peptides No. 1, 3, and 8 shown in SEQ ID NO: 4 to 6) determined from the purified SLDH polypeptide. In addition to the SLDH ORF, one more ORF, ORF2, was found just upstream of SLDH ORF as illustrated in Figs. 2 and 3. The ORF of ORF2 (381 bp, nucleotide No. 192 to 572 in SEQ ID NO: 1) encoded the polypeptide of 126 amino acid residues (SEQ ID NO: 3).

[0039] The 4th amino acid sequence of Peptide No.1 was determined as Glu by the amino acid sequencer, but it was Ala according to the DNA sequence. The 11th amino acid sequence of Peptide No.3 was determined as Gln by the amino acid sequencer, but it was Pro according to the DNA sequence. A signal peptide-like region (SEQ ID NO: 8) is possibly included in the deduced amino acid sequence: it contains (i) many hydrophobic residues, (ii) a positively-charged residues near N-terminus, and (iii) Ala-Xaa-Ala site as a cleaved signal. The actual signal sequence was determined as described in Example 3 (7). The putative ribosome-binding site (Shine-Dalgarno, SD, sequence) for SLDH gene was located at 8 bp upstream of the initiation codon (AGAGGAG at nucleotide No. 558 - 564 of Seq ID NO: 1). The putative SD sequence for ORF2 gene was located at 10 bp upstream of the initiation codon (GGGAGG at nucleotide No. 177 to 182 of Seq ID NO: 1). There were some inverted repeat sequences immediately downstream the SLDH structure gene (nucleotide sequences of No. 2803 - 2833 and of No. 2838 - 2892) as illustrated in Fig. 3; they may action as transcription termination loops for SLDH gene. For ORF2 gene, the inverted repeat sequence was found at No. 684 - 704.

[0040] Homology search for SLDH and ORF2 was performed with the programs of mpBlast (NCBI, Bethesda, Md. USA) and Motifs in GCG (Genetics Computer Group, University Research Park, WI, USA). SLDH polypeptide had the

sequence commonly conserved in quinoprotein at the region near C-terminus (within amino acid residue No. 632 to 692 of SEQ ID No. 2) and the other sequence identified as a quinoprotein motifs (Prosite No. PS00363: [DN]W.[3]G[RK].[6][FY]S.[4][LIVM]N.[2]NV.[2]L[RK]; amino acid residue No. 79 to 107 of SEQ ID No. 2).

[0041] ORF2 showed homology with the N-terminal region of the membrane-bound PQQ-dependent D-glucose dehydrogenase (GDH) of *G. oxydans*, *E. coli*, *Acinetobacter calcoaceticus*, which is known as a membrane-spanning region to bind the GDH to the membrane. Identities of ORF2 to the N-terminal region of the GDHs of *G. oxydans*, *E. coli*, *A. calcoaceticus* were 30%, 32%, and 37%, respectively. The ORF2 protein may function as an anchoring protein to make the SLDH membrane-bound type.

Example 4. Determination of N-terminal and C-terminal sequences of mature SLDH polypeptide

[0042] Direct sequencing of the N-terminus gave no results, indicating that the N-terminus is blocked. Then, SLDH polypeptide was treated with the endoproteinase Lys-C (Wako, Osaka Japan) in 0.1 M Tris-HCl at 37°C for 20 hours with a substrate-to-enzyme ratio of 20:1 (w/w). Total digest was analyzed by reversed phase HPLC (RP300, 1 mm x 25 cm, Applied Biosystems, Foster City, CA) and each peak was subjected to mass spectrometer (TSQ700 triple quadrupole instrument, Finnigan-MAT, San Jose, California) for determining molecular weight. One of the digest described as SEQ ID No. 7 was assigned as the N-terminal sequence by the mass spectrometric analysis and amino acid composition analysis together with the amino acid composition predicted from determined nucleotide sequence shown as SEQ ID NO: 1. Further analysis with collisional induced dissociation (CID) was carried out to confirm the identity of the peptide with N-terminal sequence. The N-terminus was determined to be pyroglutamyl residue.

[0043] Since the N-terminus of SLDH was determined to be Gln-Phe-Ala-Pro-Ala-Gly-Ala-Gly-Gly-Glu-Pro-Ser-Ser-Ser-Val-Pro-Gly-Pro-Gly-Asn-Ala-Ser-Glu-Pro-Thr-Glu-Asn-Ser-Pro-Lys as shown in SEQ ID NO. 7, the signal sequence was confirmed to be 24 amino acid residue long with the sequence of Met-Arg-Arg-Pro-Tyr-Leu-Leu-Ala-Thr-Ala-Ala-Gly-Leu-Ala-Leu-Ala-Cys-Ser-Pro-Leu-Ile-Ala-His-Ala as listed as SEQ ID NO: 8. The C-terminal sequence was also determined by using the peptide recovered from V8 protease digest to be Pro-Asp-Ala-Ile-Lys-Gln (SEQ ID NO: 9).

Example 5. Expression of the SLDH and/or ORF2 gene(s) in *E. coli*

[0044] From the pCRSLIP described in Example 3 (2), plasmids carrying SLDH gene with or without ORF2 gene under the lac promoter control were constructed as illustrated in Fig. 4. The resulting three plasmids are pTNB114 carrying SLDH and ORF2 genes, pTNB115 carrying SLDH gene and ORF2 gene truncated at its N-terminus containing ribosome binding site and start codon (ATG) and pTNB116 carrying mostly-truncated ORF2 gene and intact SLDH gene. These three plasmids were introduced into *E. coli* by conventional transformation. The production of the SLDH polypeptide was detected by Western-blot analysis with cell free extracts of the resulting transformants and the SLDH activity was assayed with resting cells. The resting cell reaction was carried out in the reaction mixture consisting of 0.3% NaCl, 1% CaCO₃, 4% D-sorbitol, and 1 mM PMS with or without 1 µg/ml of PQQ at room temperature for 17 hours. The SLDH activity to produce L-sorbose was analyzed by TLC assay with Silica gel 60 F₂₅₄, 0.25 mm, Merck with the developing solvent consisting of *n*-propanol-H₂O-1% H₃PO₄-HCOOH (400:100:10:1) and spray reagent of naphthoresorcinol. Consequently, SLDH polypeptide was detected in all transformants, even without ORF2 gene expression, in Western-blot analysis, but SLDH activity to produce L-sorbose was detected only in transformant carrying pTNB114 containing intact ORF2 gene under the resting cell reaction condition in the presence of PQQ.

Example 6. Expression of the SLDH and/or ORF2 gene(s) in *E. coli*

[0045] Figure 5 illustrates construction steps of pTNB110 and pTNB143. Plasmid pTNB110 carrying ORF2 and SLDH genes under control of the promoter of Enzyme A gene (pA) of DSM4025 (T. Hoshino et al., European Patent Application No. 9611500.8) was constructed by inserting *Hind* III-*Xho* I fragment containing pA, *Kpn* I-*Xho* I fragment from pTNB114 between *Hind* III-*Xho* I of pUC18. Plasmid pTNB143 carrying ORF2 and SLDH genes as independent expression units, ORF2 gene with pA and SLDH gene with pA, was constructed by inserting 0.9 kb *Sal* I fragment from pTNB141 and 3.2 kb *Hind* III-*Xho* I fragment from pTNB135 into pUC57/pCRII hybrid vector (*Sca* I-*Hind* III fragment with plac from pUC57 and *Xho* I to *Sca* I fragment without plac from pCRII) as shown in Fig. 5. The plasmids, pTNB110 and pTNB143, were introduced into *E. coli* by conventional transformation. The resulting transformants were subjected to Western-blot analysis and resting cell reaction as described in Example 5. Consequently, both of the transformants carrying pTNB110 and pTNB143 produced SLDH protein and showed SLDH activity to produce L-sorbose from D-sorbitol in the presence of PQQ.

Example 7. Expression of the SLDH gene in *G. oxydans* DSM 4025

[0046] The plasmid pTNB136 for the expression of SLDH gene in *G. oxydans* DSM 4025 having strong L-sorbose and L-sorbose dehydrogenase activities together with weak D-sorbitol dehydrogenase activity to produce L-sorbose, was constructed by inserting *Hind* III-*Xho* I fragment from pTNB135 (Fig. 5) between *Hind* III and *Xho* I sites of pVK100. The plasmid pTNB136 and its vector pVK100 were introduced by conjugal mating into strain GOBΔK, which is a mutant of *G. oxydans* DSM 4025 whose gene of Enzyme B (EP 832 974) having D-sorbitol dehydrogenase to produce L-sorbose is deleted by replacing two *Eco* RI fragments containing Enzyme B gene with kanamycin resistant gene cassette (1.28 kb *Eco* RI fragment of pUC4K; Pharmacia Uppsala, Sweden). The gene disruption was conducted by the recombinant DNA techniques well-known in the art. The resulting transconjugant, GOBΔK carrying pTNB136 or pVK100, produced 5 g/L or below 2 g/L of 2KGA in 10% D-sorbitol, respectively, by flask fermentation conducted at 30°C for 4 days (medium: 10% D-sorbitol, 1.6% urea, 0.05% glycerol, 0.25% $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 3% corn steep liquor, 6.25% baker's yeast wet cells and 1.5% CaCO_3). Western-blot analysis with anti-SLDH antibody revealed that the transconjugants carrying pTNB136 expressed the immuno-reactive SLDH polypeptides.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT

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(ii) TITLE OF INVENTION:

D-Sorbitol dehydrogenase gene

(iii) NUMBER OF SEQUENCES: 9

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: Macintosh

(C) OPERATING SYSTEM:

(D) SOFTWARE: MS word ver 5.1a

(v) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter suboxydans*

STRAIN: IFO 3255

(iv) FEATURE:

FEATURE KEY: CDS

POSITION: 192..572

SEQUENCING METHOD: E

FEATURE KEY: CDS

POSITION: 572..2794

SEQUENCING METHOD: E

ACAAATCATA CTGGCGGCGC TGTAGTGACA ATTCCGGCGG GTTAAAGAGA ATATTTTTTT 60

GGTGACAGGC CACAACAAAT TTTTGTACC TCAAACACAG TTTGTAGTA GCATTTGAAA 120

ACGAAGTCCG ATGGACCTGA ACTGAATATG GATTTACCGT CCGGAGGATT CAGTTTGGGA 180

GGCATTCGGT TATGCCAAAT CTTCAAGGTA ATAGGACTCT GACGGAGTGG CTGACGCTGC 240

EP 0 897 984 A2

TTCTCGGGGT CATCGTCCTT CTTGTGGGCC TGTTCCTCGT CATTGGGGGT GCTGACCTCG 300
 5 CGATGCTGGG CGGCTCTACC TACTATGTTT TCTGTGGCAT CCTCCTGGTT GCTAGCGGCG 360
 TATTTCATGCT CATGGGCGCG ACGCTTGGTG CCTTCCTGTA TCTGGGTGCC CTGGCCTACA 420
 CGTGGGTCTG GTCCTTCTGG GAAGTCGGTT TCAGCCCCAT CGATCTTCTG CCCCOCGCTT 480
 10 TCGGCCCCGAC CATCCTTGGC ATTCTCGTTG CCCTGACCAT TCCGGTCCTG CGCCGCATGG 540
 AAAGCCGTCG TACTCTCAGA GGAGCCGTCT GATGCGCCGG CCTTACCTTC TAGCAACAGC 600
 15 CGCAGGACTC GCCCTTGCCCT GTTCGCCGCT CATCGCTCAT GCACAGTTTG CTCCCGCAGG 660
 GGCTGGCGGC GAACCTTCCT CGTCAGTTCC TGGGCCAGGA AATGCGAGCG AGCCACCGA 720
 20 AAATCTCTCG AAAAGTCAGA GCTACTTCGC AGGACCGTCG CCCTATGCCC CGCAGGCTCC 780
 TGGCGTAAAC GCAGCCAACC TGCCGACAT TGAGTCAATC GATCCCTCGC AGGTCCCGGC 840
 CATGGCTCCG CAGCAGAGTG CCAATCCGGC ACGTGGAGAC TGGGTGCTT ACGGACGTGA 900
 25 CGATCATCAG ACGCGATACT CTCCGCTTTC GGAAATCACG CCTGAGAAGC CAAGCAAGCT 960
 CAAGGTCGCT TTCGTCTACC ACACGGGGAG TTATCCGCGT CCGGGACAGG TGAACAAATG 1020
 30 GGCCGCCGAA ACCACGCCGA TCAAGGTTGG TGACGGTCTC TACACATGTT CCGCCATGAA 1080
 CGACATCATC AAGCTGGATC CGGCTACGGG TAAGCAGATC TGGCGTCGGA ACGTGGATGT 1140
 CAAATACCAC TCCATTCCCT ATACCGCTGC CTGTAAGGGT GTGACGTATT TCACGTCCTC 1200
 35 CGTGGTGCCG GAAGGCCAGC CCTGCCACAA TCGCCTTATC GAAGGCACGC TGGATATGCG 1260
 TCTGATTGCG GTTGACGCGG AGACAGGGGA TTTCTGCCCT AATTTCGGTC ATGGTGGTCA 1320
 40 GGTCAACCTG ATGCAGGGTC TGGGTGAGTC TGTTCGGGC TTCGTCTCCA TGACGGCACC 1380
 TCCACCGGTC ATCAACGGCG TCGTGGTTGT AAACCACGAA GTGCTCGACG GTCAGCGCCG 1440
 45 CTGGGCTCCG TCCGGTGTGA TCCGTGGTTA CGATGCTGAA AGTGGCAAAT TCGTATGGGC 1500
 CTGGGACGTC AACAAATCCG GACGATCACA GCCAGCCTAC CGGGTAACCG TCATTACAGC 1560
 50 CGTGAACGC CGAATTCCTG GGCTACCTGA CAGGCGACAA CGAGGAGGGT CTCGTTTACG 1620
 TCCCAGACAG AACTCTGCTG CTGACTATTA CAGCGCCCTG CGTAGTGATG CTGAAAACAA 1680
 55

EP 0 897 984 A2

GGTGTCTCTCC GCTGTTGTCTG CCATTGACGT CAAGACGGGT TCTCCGCGCT GGGTCTTCCA 1740
5 GACGGCTCAT AAGGACGTCT GGGATTATGA CATCGGTTCA CAGGCGACCC TGATGGATAT 1800
GCCTGGCCCG GATGGCCAGA CGGTTCTCTGC TCTCATCATG CCGACCAAGC GTGGCCAGAC 1860
10 GTTCGTGCTT GACCGTCGTA CCGGCAAGCC AATTCTGCCG GTTGAAGAAC GCCCAGCTCC 1920
GTCCCCCTGGT GTTATTCCGG GTGACCCGCG TTCTCCGACG CAGCCATGGT CCGTCGGGAT 1980
GCCGGCCCTT CGCGTGCCGG ATCTGAAAGA GACAGACATG TGGGGTATGT CCCCCATCGA 2040
15 TCAGCTCTTC TGCCGTATCA AGTTCCGCCG TGCGAACTAT GTGGGTGAGT TCACACCACC 2100
GAGCGTTGAC AAGCCGTGGA TTGAATATCC GGGCTATAAC GGTGGCAGTG ACTGGGGCTC 2160
20 CATGTCTTAT GATCCGCAGT CCGGCATCCT GATTGCGAAC TGGAACATCA CACCGATGTA 2220
CGACCAGCTC GTAACCCGCA AGAAGGCAGA CTCCCTCGGC CTGATGCCGA TCGATGACCC 2280
CAACTTCAAG CCAGGTGGCG GTGGTGCCGA AGGTAACGGC GCCATGGACG GAACGCCTTA 2340
25 CGGTATCGTC GTGACACCGT TCTGGGATCA GTACACGGGC ATGATGTGCA ACCGTCCGCC 2400
CTACGGTATG ATCACAGCCA TCGACATGAA GCACGGCCAG AAGGTTCTGT GGCAGCATCC 2460
30 GCTCGGAACG GCTCGCGCCA ACGGTCCATG GGGTCTGCCA ACAGGTCTGC CATGGGAAAT 2520
CGGCACTCCG AACAAATGGT GTTCGGTTGT GACCGGTGGC GGTCTGATCT TCATCGGTGC 2580
35 GGCAACGGAT AACCAGATCC GCGCGATTGA TGAACACACT GGCAAGGTTG TCTGGAGCGC 2640
AGTCCTCCCC GCGGCGGTC AGGCCAATCC GATGACGTAT GAAGCCAATG GTCACCAGTA 2700
CGTTGCCATC ATGGCTGGCG GTCATCACTT CATGATGACG CCAGTGTCTG ACCAGCTTGT 2760
40 GGTTTACGCA CTGCCGATG CCATCAAGCA GTAATTAAGT CCTGTGGCGG ATGTGTCATG 2820
CATATCCGCC AACTCCATC GTCAGAAGGA GACTTTCGTG CTAGCCATGC AGGGAAGTCT 2880
45 CCTTTTGACG TTTTGGCTC TTTCCAGCGA GCGGGCAGTC TGAAACGGGG CTTCTGTCTG 2940
CTCGTACTTT CAGAAATGGCT CGTCGCACCC TCATGACTGC CCACTCCCCC GTTATCTTGC 3000
50 AGGTTCTGCC AGCCCTCAGC ACGGGCGGCC TGGAGCGGGG AGCTATTGAA ATTGCGGCTG 3060
CCATCACACA GGCTGGTGGC AAGGCCATTG TCGCTTCGAA GACGGGTCCT CTTCTTGTGC 3120

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EP 0 897 984 A2

AACTCCGCCA CGTCGGAGCA GTGCATGTGC CGCTGGATCT CAAATCGAAA TCGCCGTTTT 3180

5 CTGTTCCGGC CCGTGCCCGT GAACTCCAGA AACTGATCCG GGAGCAGCAG GTTGATCTGG 3240

TTCACGCCCC GTCCCGTATT CCGGCATGGG CCGCCTGGCT CGCCTGCCGC CGCGAGAACA 3300

10 TTCCTTTCGT GACAACGTGG CATGGCGTCC ACGAGGCTGG CTGGTGGGGC AAGAAATTCT 3360

ACAATTCGGT GCTGGCCCCG GGTGCAAGGG TCATCGCAAT TTCGCACTAC ATTTCCGGGC 3420

15 GTCTTTCAGG GCAGTACGGC GTTCAGGCAG ATCGTCTTCG AACCATTCCG CGTGGTGCCG 3480

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INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 740 residues

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter suboxydans*

STRAIN: IFO 3255

(iv) FEATURE:

FEATURE KEY: sig peptide

POSITION: -24..-1

SEQUENCING METHOD: E

FEATURE KEY: mat peptide

POSITION: 1..716

SEQUENCING METHOD: E

Met Arg Arg Pro Tyr Leu Leu Ala Thr Ala Ala Gly Leu Ala Leu

-24 -20 -15 -10

Ala Cys Ser Pro Leu Ile Ala His Ala Gln Phe Ala Pro Ala Gly

-5 1 5

EP 0 897 984 A2

	Ala Gly Gly Glu Pro Ser Ser Ser Val Pro Gly Pro Gly Asn Ala
5	10 15 20
	Ser Glu Pro Thr Glu Asn Ser Pro Lys Ser Gln Ser Tyr Phe Ala
10	25 30 35
	Gly Pro Ser Pro Tyr Ala Pro Gln Ala Pro Gly Val Asn Ala Ala
15	40 45 50
	Asn Leu Pro Asp Ile Glu Ser Ile Asp Pro Ser Gln Val Pro Ala
20	55 60 65
	Met Ala Pro Gln Gln Ser Ala Asn Pro Ala Arg Gly Asp Trp Val
25	70 75 80
	Ala Tyr Gly Arg Asp Asp His Gln Thr Arg Tyr Ser Pro Leu Ser
30	85 90 95
	Glu Ile Thr Pro Glu Asn Ala Ser Lys Leu Lys Val Ala Phe Val
35	100 105 110
	Tyr His Thr Gly Ser Tyr Pro Arg Pro Gly Gln Val Asn Lys Trp
40	115 120 125
	Ala Ala Glu Thr Thr Pro Ile Lys Val Gly Asp Gly Leu Tyr Thr
45	130 135 140
	Cys Ser Ala Met Asn Asp Ile Ile Lys Leu Asp Pro Ala Thr Gly
50	145 150 155
	Lys Gln Ile Trp Arg Arg Asn Val Asp Val Lys Tyr His Ser Ile
55	160 165 170

	Pro Tyr Thr Ala Ala Cys Lys Gly Val Thr Tyr Phe Thr Ser Ser	
5	175	180 185
	Val Val Pro Glu Gly Gln Pro Cys His Asn Arg Leu Ile Glu Gly	
10	190	195 200
	Thr Leu Asp Met Arg Leu Ile Ala Val Asp Ala Glu Thr Gly Asp	
15	205	210 215
	Phe Cys Pro Asn Phe Gly His Gly Gly Gln Val Asn Leu Met Gln	
20	220	225 230
	Gly Leu Gly Glu Ser Val Pro Gly Phe Val Ser Met Thr Ala Pro	
25	235	240 245
	Pro Pro Val Ile Asn Gly Val Val Val Val Asn His Glu Val Leu	
30	250	255 260
	Asp Gly Gln Arg Arg Trp Ala Pro Ser Gly Val Ile Arg Gly Tyr	
35	265	270 275
	Asp Ala Glu Ser Gly Lys Phe Val Trp Ala Trp Asp Val Asn Asn	
40	280	285 290
	Ser Gly Arg Ser Gln Pro Ala Tyr Arg Val Thr Val Ile Thr Ala	
45	295	300 305
	Val Glu Arg Arg Ile Pro Gly Leu Pro Asp Arg Arg Gln Arg Gly	
50	310	315 320
	Gly Ser Arg Leu Arg Pro Asp Arg Asn Ser Ala Ala Asp Tyr Tyr	
55	325	330 335

	Ser Ala Leu Arg Ser Asp Ala Glu Asn Lys Val Ser Ser Ala Val	
5	340	345 350
	Val Ala Ile Asp Val Lys Thr Gly Ser Pro Arg Trp Val Phe Gln	
10	355	360 365
	Thr Ala His Lys Asp Val Trp Asp Tyr Asp Ile Gly Ser Gln Ala	
15	370	375 380
	Thr Leu Met Asp Met Pro Gly Pro Asp Gly Gln Thr Val Pro Ala	
20	385	390 395
	Leu Ile Met Pro Thr Lys Arg Gly Gln Thr Phe Val Leu Asp Arg	
25	400	405 410
	Arg Thr Gly Lys Pro Ile Leu Pro Val Glu Glu Arg Pro Ala Pro	
30	415	420 425
	Ser Pro Gly Val Ile Pro Gly Asp Pro Arg Ser Pro Thr Gln Pro	
35	430	435 440
	Trp Ser Val Gly Met Pro Ala Leu Arg Val Pro Asp Leu Lys Glu	
	D-Sorbitol dehydrogenase gene	445
40	450	455
	Thr Asp Met Trp Gly Met Ser Pro Ile Asp Gln Leu Phe Cys Arg	
45	460	465 470
	Ile Lys Phe Arg Arg Ala Asn Tyr Val Gly Glu Phe Thr Pro Pro	
50	475	480 485
	Ser Val Asp Lys Pro Trp Ile Glu Tyr Pro Gly Tyr Asn Gly Gly	
55	490	495 500

	Ser Asp Trp Gly Ser Met Ser Tyr Asp Pro Gln Ser Gly Ile Leu	
5	505	510 515
	Ile Ala Asn Trp Asn Ile Thr Pro Met Tyr Asp Gln Leu Val Thr	
10	520	525 530
	Arg Lys Lys Ala Asp Ser Leu Gly Leu Met Pro Ile Asp Asp Pro	
15	535	540 545
	Asn Phe Lys Pro Gly Gly Gly Gly Ala Glu Gly Asn Gly Ala Met	
20	550	555 560
	Asp Gly Thr Pro Tyr Gly Ile Val Val Thr Pro Phe Trp Asp Gln	
25	565	570 575
	Tyr Thr Gly Met Met Cys Asn Arg Pro Pro Tyr Gly Met Ile Thr	
30	580	585 590
	Ala Ile Asp Met Lys His Gly Gln Lys Val Leu Trp Gln His Pro	
35	595	600 605
	Leu Gly Thr Ala Arg Ala Asn Gly Pro Trp Gly Leu Pro Thr Gly	
40	610	615 620
	Leu Pro Trp Glu Ile Gly Thr Pro Asn Asn Gly Gly Ser Val Val	
45	625	630 635
	Thr Gly Gly Gly Leu Ile Phe Ile Gly Ala Ala Thr Asp Asn Gln	
50	640	645 650
	Ile Arg Ala Ile Asp Glu His Thr Gly Lys Val Val Trp Ser Ala	
55	655	660 665

5	Val	Leu	Pro	Gly	Gly	Gly	Gln	Ala	Asn	Pro	Met	Thr	Tyr	Glu	Ala
				670					675					680	
10	Asn	Gly	His	Gln	Tyr	Val	Ala	Ile	Met	Ala	Gly	Gly	His	His	Phe
				685					690					695	
15	Met	Met	Thr	Pro	Val	Ser	Asp	Gln	Leu	Val	Val	Tyr	Ala	Leu	Pro
				700					705					710	
20	Asp	Ala	Ile	Lys	Gln										
				715	716										

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INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 residues

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) FRAGMENT TYPE: internal fragment

(iv) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter suboxydans*

STRAIN: IFO 3255

(v) FEATURE:

FEATURE KEY: mat peptide

POSITION: 1..126

SEQUENCING METHOD: E

Met Pro Asn Leu Gln Gly Asn Arg Thr Leu Thr Glu Trp Leu Thr

1 5 10 15

Leu Leu Leu Gly Val Ile Val Leu Leu Val Gly Leu Phe Phe Val

20 25 30

Ile Gly Gly Ala Asp Leu Ala Met Leu Gly Gly Ser Thr Tyr Tyr

35 40 45

Val Leu Cys Gly Ile Leu Leu Val Ala Ser Gly Val Phe Met Leu

50 55 60

	Met	Gly	Arg	Thr	Leu	Gly	Ala	Phe	Leu	Tyr	Leu	Gly	Ala	Leu	Ala	
5					65				70						75	
	Tyr	Thr	Trp	Val	Trp	Ser	Phe	Trp	Glu	Val	Gly	Phe	Ser	Pro	Ile	
10					80				85						90	
	Asp	Leu	Leu	Pro	Arg	Ala	Phe	Gly	Pro	Thr	Ile	Leu	Gly	Ile	Leu	
15					95				100						105	
	Val	Ala	Leu	Thr	Ile	Pro	Val	Leu	Arg	Arg	Met	Glu	Ser	Arg	Arg	
20					110				115						120	
	Thr	Leu	Arg	Gly	Ala	Val										
25					125	126										

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INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 residues

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) FRAGMENT TYPE: internal fragment

(iv) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter suboxydans*

STRAIN: IFO 3255

(v) FEATURE:

SEQUENCING METHOD: E

Lys Trp Ala Glu Glu Thr Xaa Pro

1

5

8

INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 residues

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) FRAGMENT TYPE: internal fragment

(iv) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter suboxydans*

STRAIN: IFO 3255

(v) FEATURE:

SEQUENCING METHOD: E

Lys Ser Gln Ser Tyr Phe Ala Gly Pro Ser Gln Tyr Ala Pro Gln

1 5 10 15

Ala Pro Gly Val Asn Ala Xaa Asn Leu

20 24

INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 residues

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) FRAGMENT TYPE: internal fragment

(iv) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter suboxydans*

STRAIN: IFO 3255

(v) FEATURE:

SEQUENCING METHOD: E

Lys Val Leu Trp Gln His Pro Leu Gly Thr Ala Arg Xaa Asn Gly

1

5

10

15

Pro

16

INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 residues

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) FRAGMENT TYPE: N-terminal fragment

(iv) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter suboxydans*

STRAIN: IFO 3255

(v) FEATURE:

SEQUENCING METHOD: E

Gln Phe Ala Pro Ala Gly Ala Gly Gly Glu Pro Ser Ser Ser Val

1 5 10 15

Pro Gly Pro Gly Asn Ala Ser Glu Pro Thr Glu Asn Ser Pro Lys

20 25 30

INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 residues

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter suboxydans*

STRAIN: IFO 3255

(iv) FEATURE:

FEATURE KEY: sig peptide

POSITION: 1..24

SEQUENCING METHOD: E

Met Arg Arg Pro Tyr Leu Leu Ala Thr Ala Ala Gly Leu Ala Leu

1

5

10

15

Ala Cys Ser Pro Leu Ile Ala His Ala

20

24

INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 residues

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) FRAGMENT TYPE: C-terminal fragment

(iv) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter suboxydans*

STRAIN: IFO 3255

(v) FEATURE:

SEQUENCING METHOD: E

Pro Asp Ala Ile Lys Gln

1 5 6

50 Claims

1. A DNA comprising a nucleotide sequence which encodes a protein as defined by (a) or (b) and having sorbitol dehydrogenase activity:

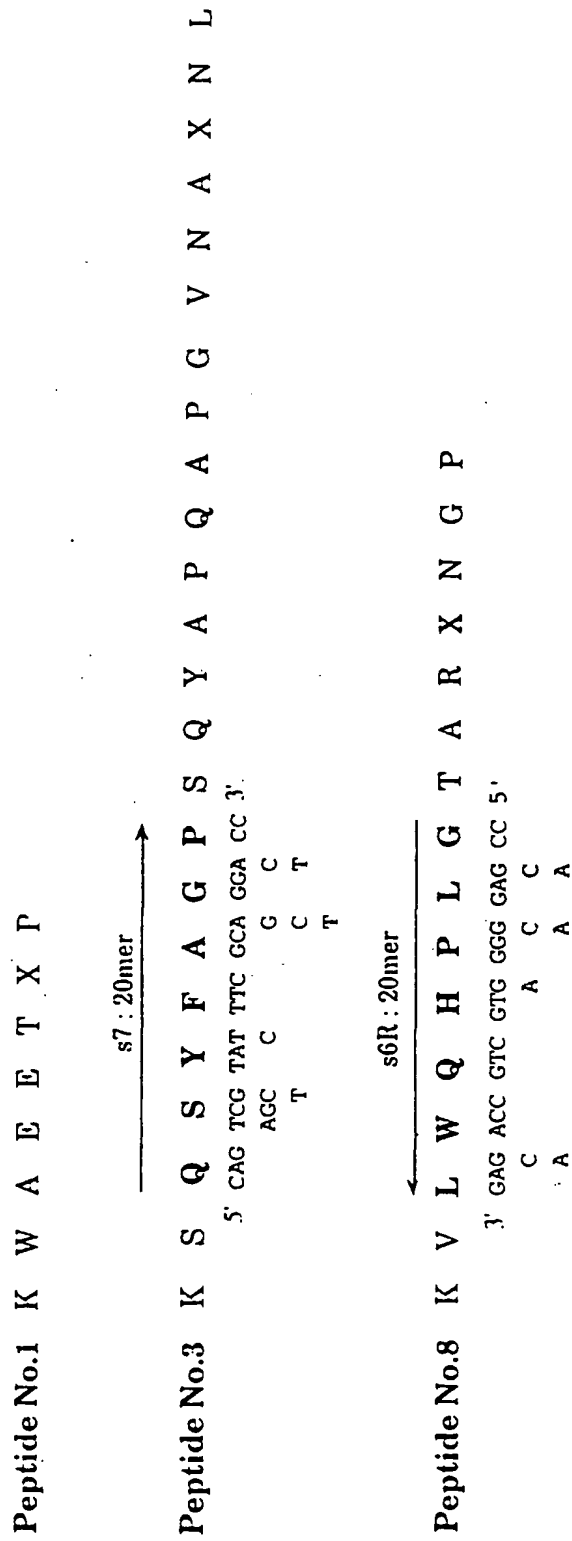
(a) a protein having the amino acid sequence from the position 1 to 716 of the sequence described in SEQ ID NO: 2, or

(b) a protein derived from the protein of (a) by substitution, deletion, insertion or addition of one or more amino

acids in the amino acid sequence defined in (a).

2. A DNA according to claim 1, which encodes sorbitol dehydrogenase of a microorganism belonging to acetic acid bacteria.
3. A DNA according to claim 2, wherein the said microorganism belongs to the genus *Gluconobacter* or the genus *Acetobacter*.
4. A DNA according to any one of claims 1-4, which is selected from the group consisting of:
 - (e) a DNA comprising a nucleotide sequence from the position 644 to 2791 or from the position 572 to 2791 of the sequence represented by SEQ ID NO: 1, and
 - (f) a DNA which is capable of hybridizing to the DNA defined in (e) and encodes the protein having the function of the protein defined in (a) of claim 1.
5. A combination of DNAs comprising:
 - (1) a DNA as defined in any one of claims 1-4; and
 - (2) a DNA encoding ORF2 having a nucleotide sequence from the position 192 to 569 of the sequence represented by SEQ ID NO: 1 and/or a DNA encoding an ORF2 derivative with substitution, deletion, insertion or addition of one or more amino acids of the sequence defined in SEQ ID NO: 3 and with the function equivalent to the one of ORF2.
6. A combination of DNAs according to claim 5 comprising:
 - (1) a DNA having a nucleotide sequence from the position 644 to 2791 or from the position 572 to 2791 of the sequence represented by SEQ ID NO: 1; or a DNA which is capable of hybridizing to this DNA which encodes the protein having the function of the protein defined claim 1; and
 - (2) a DNA encoding ORF2 having a nucleotide sequence from the position 192 to 569 of the sequence represented by SEQ ID NO: 1 or a DNA encoding an ORF2 derivative with substitution, deletion, insertion or addition of one or more amino acids of the sequence defined in SEQ ID NO: 3 with the function equivalent to one of ORF2.
7. An expression vector comprising a DNA as claimed in any one of claims 1 - 6.
8. A combination of DNAs according to claims 5 or 6, wherein the respective DNAs are separately carried on different expression vectors or on the same expression vector.
9. A combination of DNAs according to claims 5 or 6, which are in a tandem form as described in SEQ ID NO: 1.
10. The expression vector of claim 7, which is functional in a microorganism selected from those belonging to the genus *Gluconobacter*, *Acetobacter* or *E. coli*.
11. A recombinant organism which has been transformed by an expression vector as claimed in any one of claims 7 to 10.
12. A recombinant organism having the DNA as claimed in any one of claims 1 - 4 or the combination of the DNAs as defined in any one of claims 5, 6, 8 or 9 on a chromosomal DNA of the host organism.
13. The recombinant organism as claimed in claim 11 or 12, wherein the host organism is a microorganism selected from those belonging to the genus *Gluconobacter*, *Acetobacter* or *E. coli*.
14. A process for producing recombinant D-sorbitol dehydrogenase which comprises cultivating the recombinant organism as claimed in any one of claims 11 - 13 in an appropriate medium and recovering the said recombinant D-sorbitol dehydrogenase from the culture.

15. A recombinant D-sorbitol dehydrogenase produced by the expression of the DNA as claimed in any one of claims 1 - 4 or a combination of DNAs as claimed in any one of claims 5, 6, 8 or 9.
16. A recombinant D-sorbitol dehydrogenase produced by the process claimed in claim 14.
17. A recombinant D-sorbitol dehydrogenase according to claim 15 or 16, which is immobilized on a solid carrier for solid phase enzymatic reaction.
18. A process for producing L-sorbose which comprises converting D-sorbitol into L-sorbose with the aid of the recombinant D-sorbitol dehydrogenase claimed in claim 16 or 17..
19. A process for producing L-sorbose which comprises converting D-sorbitol into L-sorbose by fermentation of the recombinant organism claimed in any one of claims 11 - 13 in an appropriate medium.



The amino acid sequence in boldface were used for synthesizing two oligonucleotide sequences (S7 and s6R) for PCR. Arrows show direction of DNA synthesis. The primers were degenerate DNA mixtures having bias for *Gluconobacter* codon usage.

Fig. 1

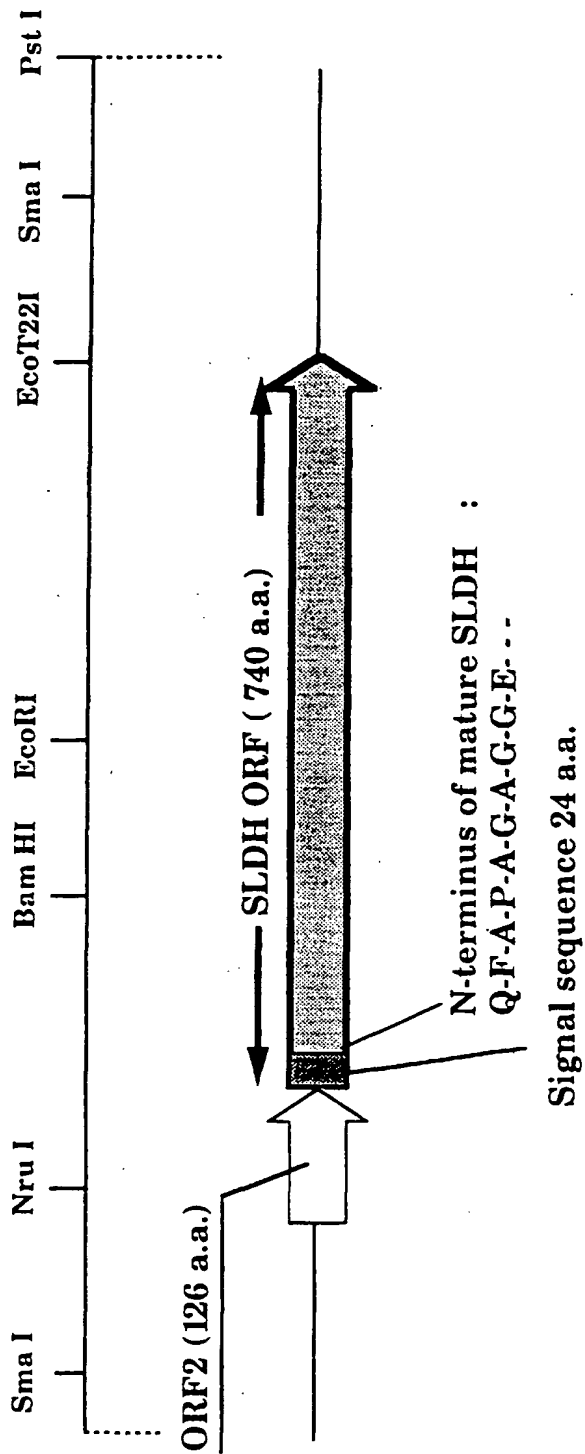


Fig. 2

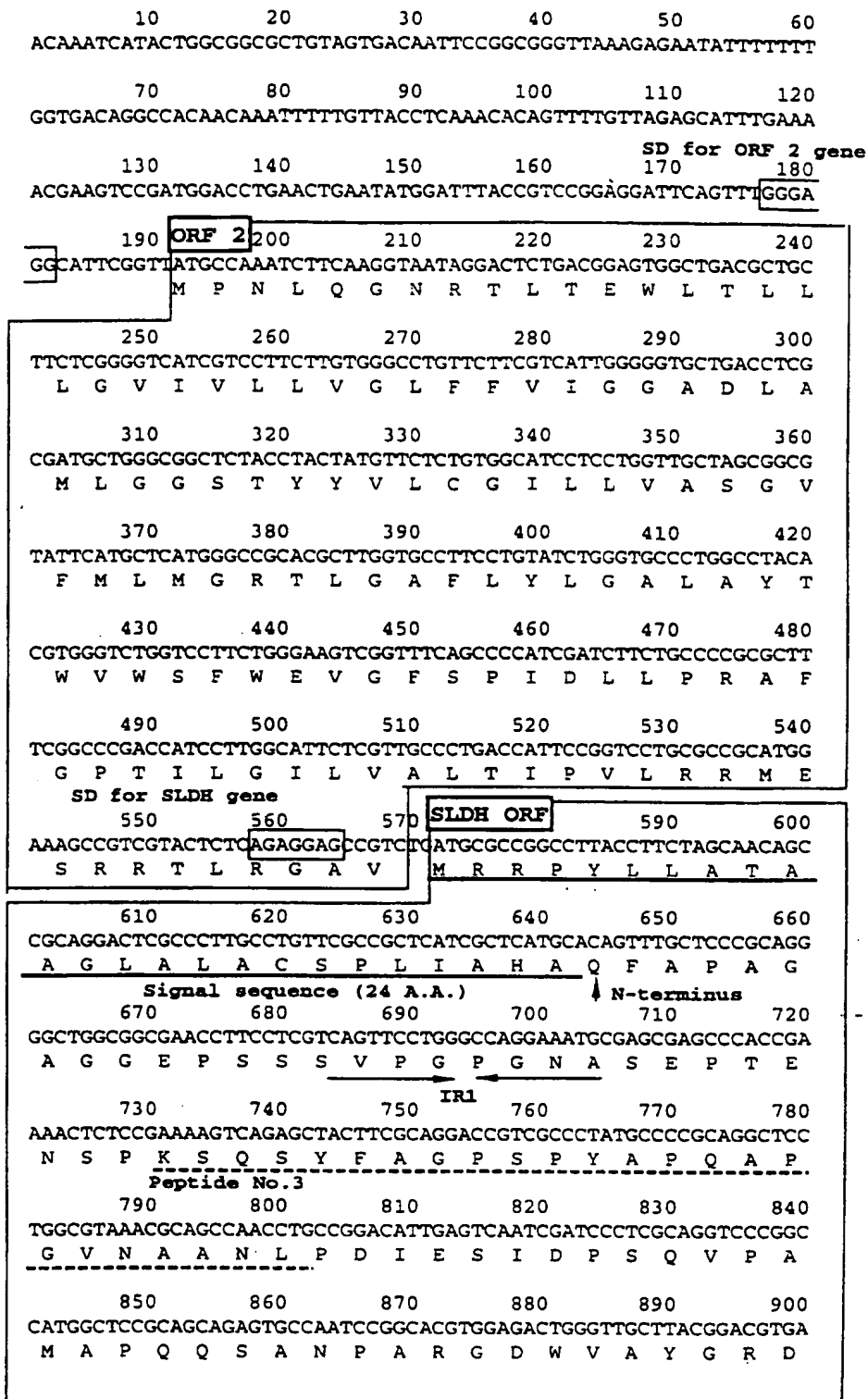


Fig. 3a

910	920	930	940	950	960
CGATCATCAGACGCGATACTCTCCGCTTTTCGGAATCAGGCCTGAGAACGCAAGCAAGCT					
D H Q T R Y S P L S E I T P E N A S K L					
970	980	990	1000	1010	1020
CAAGGTCGCTTTTCGTCTACACACGGGGAGTTATCCGCGTCCGGGACAGGTGAACAAATG					
K V A F V Y H T G S Y P R P G Q V N K W					
				Peptide No.1	
1030	1040	1050	1060	1070	1080
GGCCGCCGAAACCACGCCGATCAAGGTTGGTGACGGTCTCTACACATGTTCCGCCATGAA					
A A E T T P I K V G D G L Y T C S A M N					

1090	1100	1110	1120	1130	1140
CGACATCATCAAGCTGGATCCGGCTACGGGTAAGCAGATCTGGCGTCGGAACGTGGATGT					
D I I K L D P A T G K Q I W R R N V D V					
1150	1160	1170	1180	1190	1200
CAAATACCACTCCATTCCCTATACCGCTGCCTGTAAGGGTGTGACGTATTTACGTCCTC					
K Y H S I P Y T A A C K G V T Y F T S S					
1210	1220	1230	1240	1250	1260
CGTGGTGC CGGAGGCCAGCCCTGCCACAATCGCCTTATCGAAGGCACGCTGGATATGCG					
V V P E G Q P C H N R L I E G T L D M R					
1270	1280	1290	1300	1310	1320
TCTGATTGCGGTGACGCGGAGACAGGGGATTTCTGCCCTAATTTTCGGTCATGCTGGTCA					
L I A V D A E T G D F C P N F G H G G Q					
1330	1340	1350	1360	1370	1380
GGTCAACCTGATGCAGGGTCTGGGTGAGTCTGTTCCGGGCTTCGTCCTCCATGACGGCACC					
V N L M Q G L G E S V P G F V S M T A P					
1390	1400	1410	1420	1430	1440
TCCACCGGTCATCAACGGCGTCGTGGTTGTAACCACGAAGTGCTCGACGGTCAGCGCCG					
P P V I N G V V V V N H E V L D G Q R R					
1450	1460	1470	1480	1490	1500
CTGGGCTCCGTCGGTGTGATCCGTGGTTACGATGCTGAAAGTGGCAAATTCGTATGGGC					
W A P S G V I R G Y D A E S G K F V W A					
1510	1520	1530	1540	1550	1560
CTGGGACGTCAACAATTCCGGACGATCACAGCCAGCCTACCGGTAACCGTCATTACAGC					
W D V N N S G R S Q P A Y R V T V I T A					
1570	1580	1590	1600	1610	1620
CGTGGAACGCCGAATTCCTGGGCTACCTGACAGGCGACAACGAGGAGGGTCTCGTTTACG					
V E R R I P G L P D R R Q R G G S R L R					
1630	1640	1650	1660	1670	1680
TCCCGACAGGAATCTGCTGCTGACTATTACAGCGCCCTGCGTAGTGATGCTGAAAACAA					
P D R N S A A D Y Y S A L R S D A E N K					
1690	1700	1710	1720	1730	1740
GGTGTCTCCGCTGTTGTCGCCATTGACGTCAAGACGGGTCTCCGCGCTGGGTCTTCCA					
V S S A V V A I D V K T G S P R W V F Q					
1750	1760	1770	1780	1790	1800
GACGGCTCATAAGGACGTCTGGGATTATGACATCGGTTACAGGCGACCCTGATGGATAT					
T A H K D V W D Y D I G S Q A T L M D M					

Fig. 3b

1810	1820	1830	1840	1850	1860
GCCTGGCCCGGATGGCCAGACGGTTCCTGCTCTCATCATGCCGACCAAGCGTGGCCAGAC					
P G P D G Q T V P A L I M P T K R G Q T					
1870	1880	1890	1900	1910	1920
GTTCTGCTTGACCGTCGTACCGGCAAGCCAATTCTGCCGGTTGAAGAAGCCCCAGCTCC					
F V L D R R T G K P I L P V E E R P A P					
1930	1940	1950	1960	1970	1980
GTCCCTGGTGTATTCCGGGTGACCCGCGTTCCTCCGACGCAGCCATGGTCCGTCCGGGAT					
S P G V I P G D P R S P T Q P W S V G M					
1990	2000	2010	2020	2030	2040
GCCGGCCCTTCGCGTCCCGGATCTGAAAGAGACAGACATGTGGGGTATGTCCCCCATCGA					
P A L R V P D L K E T D M W G M S P I D					
2050	2060	2070	2080	2090	2100
TCAGCTCTTCTGCCGTATCAAGTTCGCGCGTGCAGTATGTGGGTGAGTTCACACCACC					
Q L F C R I K F R R A N Y V G E F T P P					
2110	2120	2130	2140	2150	2160
GAGCGTTGACAAGCCGTGGATTGAATATCCGGGCTATAACGGTGGCAGTGACTGGGGCTC					
S V D K P W I E Y P G Y N G G S D W G S					
2170	2180	2190	2200	2210	2220
CATGTCCTATGATCCGCAGTCCGGCATCCTGATTGCGAACTGGAACATCACACCGATGTA					
M S Y D P Q S G I L I A N W N I T P M Y					
2230	2240	2250	2260	2270	2280
CGACCAGCTCGTAACCCGCAAGAAGGCAGACTCCCTCGGCCTGATGCCGATCGATGACCC					
D Q L V T R K K A D S L G L M P I D D P					
2290	2300	2310	2320	2330	2340
CAACTTCAAGCCAGGTGGCGGTGGTGCAGGTAACGGCGCCATGGACGGAACGCCTTA					
N F K P G G G G A E G N G A M D G T P Y					
2350	2360	2370	2380	2390	2400
CGGTATCTGTCGTGACACCGTTCTGGGATCAGTACACGGGCATGATGTGCAACCGTCCGCC					
G I V V T P F W D Q Y T G M M C N R P P					
2410	2420	2430	2440	2450	2460
CTACGGTATGATCACAGCCATCGACATGAAGCACGGCCAGAAGGTTCTGTGGCAGCATCC					
Y G M I T A I D M K H G Q <u>K V L W Q H P</u>					
2470	2480	2490	2500	2510	2520
GCTCGGAACGGCTCGCGCAACGGTCCATGGGGTCTGCCAACAGGTCTGCCATGGGAAAT					
L G T A R A N G P W G L P T G L P W E I					
2530	2540	2550	2560	2570	2580
CGGCACCTCCGAACAATGGTGGTTCGGTTGTGACCGGTGGCGGTCTGATCTTCATCGGTGC					
G T P N N G G S V V T G G G L I F I G A					
2590	2600	2610	2620	2630	2640
GGCAACGGATAACCAGATCCGCGGATTTGATGAACACACTGGCAAGGTTGTCTGGAGCGC					
A T D N Q I R A I D E H T G K V V W S A					
2650	2660	2670	2680	2690	2700
AGTCCTCCCGGCGCGGTCAGGCCAATCCGATGACGTATGAAGCCAATGGTCACCACTA					
V L P G G G Q A N P M T Y E A N G H Q Y					

Fig. 3c

2710	2720	2730	2740	2750	2760
CGTTGCCATCATGGCTGGCGGTCATCACTTCATGATGACGCCAGTGTCTGACCAGCTTGT					
V A I M A G G H H F M M T P V S D Q L V					

2770	2780	2790	2800	2810	2820
GGTTTACGCACTGCCGGATGCCATCAAGCAGTAATTAAGTCCTGTGGCGGATGTGTCATG					
V Y A L P D A I K Q					

IR2

2830	2840	2850	2860	2870	2880
CATATCCGCCACACTCCATCGTCAGAAGGAGACTTTCTGTCTAGCCATGCAGGGAAGTCT					

2890	2900	2910	2920	2930	2940
CCTTTTGACGTTTTTTGGCTCTTTCCAGCGAGCGGGCAGTCTGAAACGGGGCTTCGTCTGG					

IR2'

2950	2960	2970	2980	2990	3000
CTCGTACTTTTCAGAATGGCTCGTCGCACCCCTCATGACTGCCCCACTCCCCCGTTATCTTGC					

3010	3020	3030	3040	3050	3060
AGGTTCTGCCAGCCCTCAGCACGGGCGGCCTGGAGCGGGAGCTATTGAAATTGCGGCTG					

3070	3080	3090	3100	3110	3120
CCATCACACAGGCTGGTGGCAAGGCCATTGTGCGTTTGAAGACGGGTCTCTTCTTGTGC					

3130	3140	3150	3160	3170	3180
AACTCCGCCACGTGCGGAGCAGTGCATGTGCCGCTGGATCTCAAATCGAAATCGCCGTTTT					

3190	3200	3210	3220	3230	3240
CTGTTTCGGCGCCGTGCCCGTGAAGTCCAGAACTGATCCGGGAGCAGCAGGTTGATCTGG					

3250	3260	3270	3280	3290	3300
TTCACGCCCCGTCCCGTATTCCGGCATGGGCCGCTGGCTCGCCTGCCGCCGCGAGAACA					

3310	3320	3330	3340	3350	3360
TTCTTTTCGTGACAACGTGGCATGGCGTCCACGAGGCTGGCTGGTGGGGCAAGAAATTCT					

3370	3380	3390	3400	3410	3420
ACAATTGGGTGCTGGCCCCGGGTGCAAGGGTCATCGCAATTTGCGACTACATTTCCGGGC					

3430	3440	3450	3460	3470	3480
GTCTTTCAGGGCAGTACGGCGTTTCAGGCAGATCGTCTTGAACCATTCGCGTGGTGCCG					

3481

A

————— : IR1 and IR2 (or 2') are inverted repeats as possible transcription terminators for ORF2 and SLDH II genes, respectively.

Fig. 3d

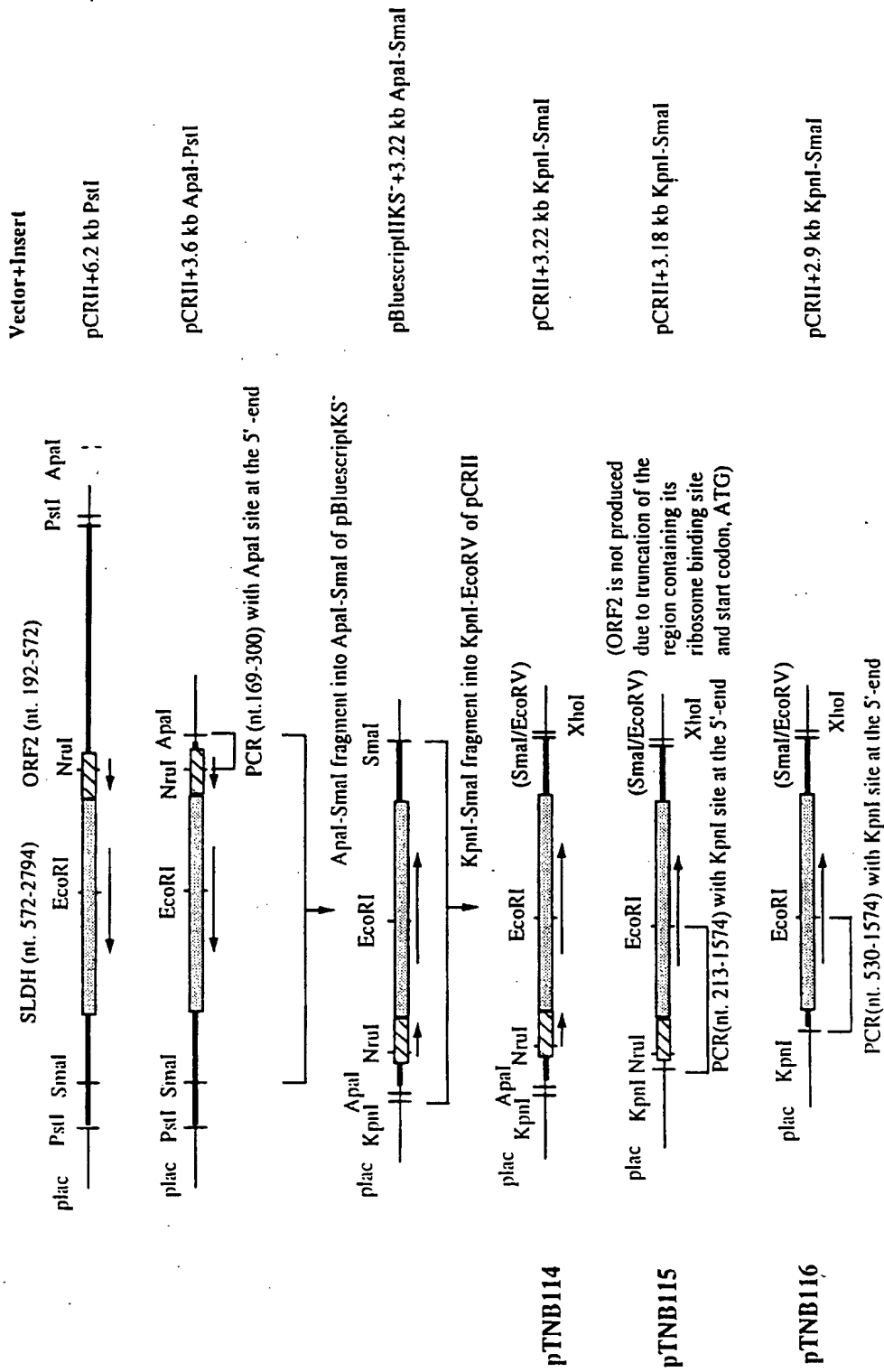


Fig. 4

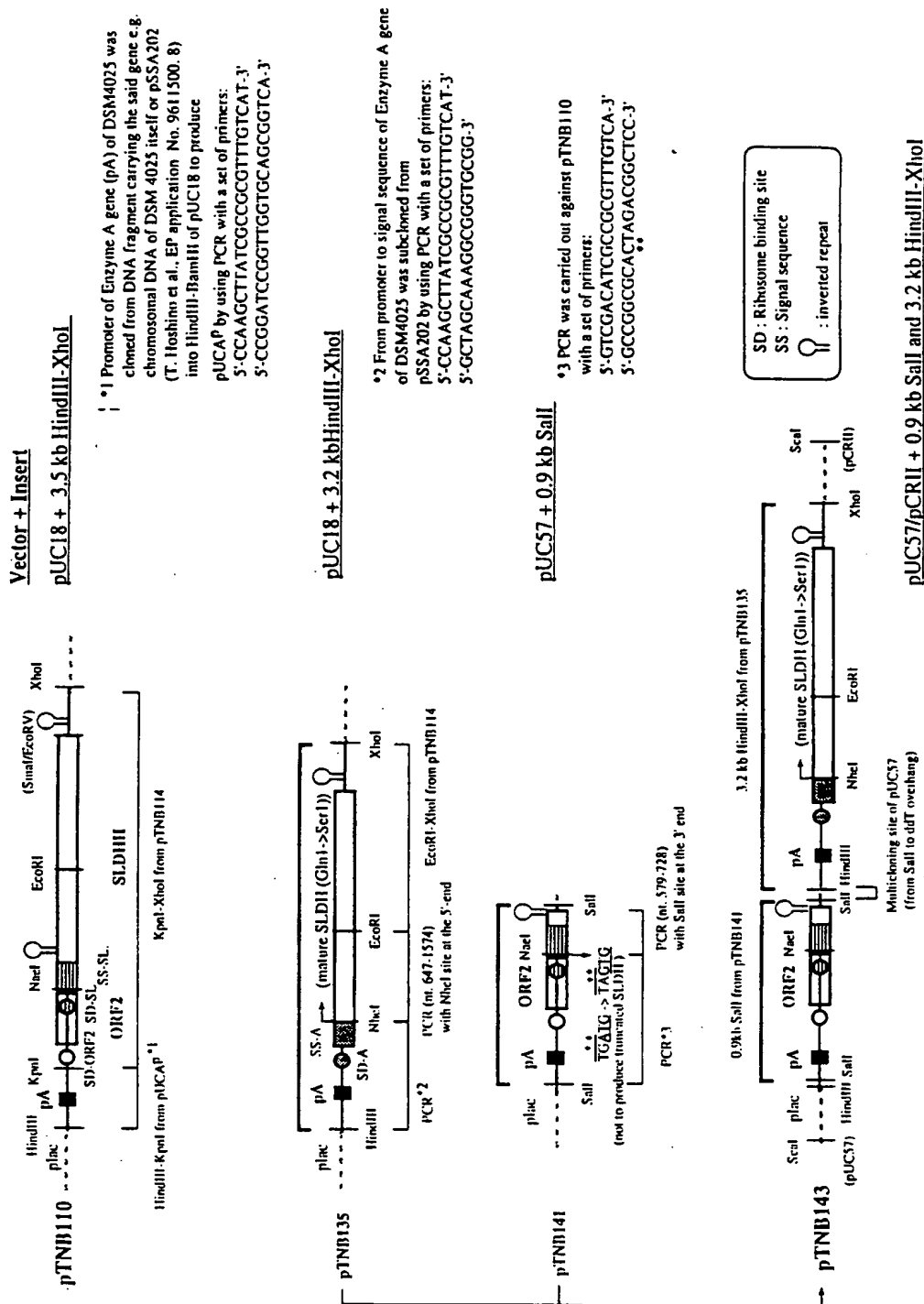


Fig. 5.